OM protein - protein search, using sw model

GenCore version 5.1.3
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Run on: March 14, 2003, 05:30:50 ; Search time 50.2472 Seconds
                                     (without alignments)
                                     1057.973 Million cell updates/sec

Title: US-09-698-781-3
Perfect score: 1436
Sequence: 1 MKQILHPALETTAMTLFPVL.........KHQLVRDSCKASCNCSNSIY 258

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Post-processing: Minimum Match 0%
                 Maximum DB seq length: 2000000000
                 Listing first 45 summaries

Database :   SPTREMBL_21:*
          1:    sp_archea:*
          2:    sp_bacteria:*
          3:    sp_fungi:*
          4:    sp_human:*
          5:    sp_invertebrate:*
          6:    sp_mammal:*
          7:    sp_mhc:*
          8:    sp_organelle:*
          9:    sp_phage:*
         10:    sp_plant:*
         11:    sp_rodent:*
         12:    sp_virus:*
         13:    sp_vertebrate:*
         14:    sp_unclassified:*
         15:    sp_rvirus:*
         16:    sp_bacterial:*
         17:    sp_archeap:*

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1127	78.5	203	4	Q9H108	q9h108 homo sapien
2	852	59.3	243	11	O88205	o88205 rattus norv
3	849	59.1	243	11	Q9R1L4	q9r1l4 rattus norv
4	754.5	52.5	244	11	Q91XA3	q91xa3 mus musculu
5	684	47.6	165	6	Q77720	q77720 equus cabal
6	590.5	41.1	151	6	Q9N0J2	q9n0j2 equus cabal
7	574.5	40.0	250	11	Q9D259	q9d259 mus musculu
8	542.5	37.8	249	6	Q9XSD3	q9xsd3 macaca mula
9	525	36.6	217	6	O77719	o77719 equus cabal
10	520	36.7	181	13	Q8UW11	q8uw11 lapemis har
11	512.5	35.7	199	13	Q8UW25	q8uw25 lapemis har
12	463	32.2	111	6	Q9N0J1	q9n0j1 bos taurus
13	440	30.6	158	11	Q9R0V8	q9r0v8 rattus norv
14	373.5	26.0	178	4	Q96SF6	q96sf6 homo sapien
15	358	24.9	153	13	Q90XE5	q90xe5 xenopus lae
16	345	24.0	79	6	O77818	o77818 sus scrofa
17	344	24.0	255	11	Q9CWG1	q9cwg1 mus musculu
18	328	22.8	266	4	Q969K2	q969k2 homo sapien
19	311.5	21.7	489	11	Q9JJ56	q9jj56 mus musculu
20	311.5	21.5	489	11	Q9ET66	q9et66 mus musculu
21	308.5	21.5	236	11	Q9DAG6	q9dag6 mus musculu
22	305.5	21.3	233	4	Q96L06	q96l06 homo sapien
23	295.5	20.6	371	4	Q96K61	q96k61 homo sapien
24	295.5	20.6	497	4	Q9H0B8	q9h0b8 homo sapien
25	292	20.3	258	11	Q99MM7	q99mm7 mus musculu
26	291	20.3	415	4	Q8TCB8	q8tcb8 homo sapien
27	290	20.2	258	4	O43692	o43692 homo sapien
28	288.5	20.1	380	5	Q9VFY2	q9vfy2 drosophila
29	288.5	20.1	392	5	Q960R5	q960r5 drosophila
30	288.5	20.1	500	4	Q9H336	q9h336 homo sapien
31	286	19.9	258	13	Q98ST6	q98st6 gallus gall
32	285.5	19.9	523	13	Q98ST5	q98st5 gallus gall
33	280.5	19.5	434	11	Q9D2R3	q9d2r3 mus musculu
34	279.5	19.5	507	13	Q99MM6	q99mm6 mus musculu
35	278	19.4	188	11	Q92U06	q92u06 mus musculu
36	277	19.3	424	4	O76744	o76744 necator ame
37	277	19.3	424	5	Q9X241	q9x241 ancylostoma
38	274.5	19.1	100	11	Q9D2T2	q9d2t2 mus musculu
39	263	18.3	425	5	O77153	o77153 ancylostoma
40	258.5	18.0	332	11	Q9CQ35	q9cq35 mus musculu
41	256.5	17.9	301	5	Q5SOF6	q5sof6 caenorhabdi
42	255	17.8	253	4	Q9H3Y0	q9h3y0 homo sapien
43	252.5	17.6	207	5	Q20603	q20603 caenorhabdi
44	249	17.3	208	5	Q9N5N3	q9n5n3 caenorhabdi
45	248.5	17.3	415	5	O44228	o44228 halocynthia

RESULT 1
Q9H108

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ID   Q9H108      PRELIMINARY;    PRT;   203 AA.
AC   Q9H108;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   DJ417L20.1 (Cysteine-rich secretory protein 3 (Crisp-3, SGP28))
DE   (Fragment).
GN   DJ417L20.1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Phillimore B.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL121974; CAC19654.1; -.
DR   HSSP; P04284; 1CFE.
DR   InterPro; IPR001283; Allrgn_V5/Tpxl.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpxl; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
FT   NON_TER      1      1.
SQ   SEQUENCE   203 AA;  22912 MW;  F80D707EE0D81A2B CRC64;
```

ALIGNMENTS

Query Match   78.5%;   Score 1127;   DB 4;   Length 203;
Best Local Similarity 99.5%; Pred. No. 1.8e-101;
Matches 202; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

```
Qy    14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     1 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 60

Qy    74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRWTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
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Db   61 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSASSSWSQAIQSWFDEY 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  134 NDFDFGVGPKTPNAVVGHYTQVVWYSSILVGGGNAYCPNQKVLKYYVCQYCPAGNWANR 193
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 NDFDFGVGPKTPNAVVGHYTQVVWYSSILVGGGNAYCPNQKVLKYYVCQYCPAGNWANR 180

Qy  194 LYVPYEQGAPCASCPDNCDDGLC 216
         |||||||||||||||||||||||
Db  181 LYVPYEQGAPCASCPDNCDDGLC 203
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RESULT 2
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ID   O88205        PRELIMINARY;    PRT;   243 AA.
AC   O88205;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Testis specific protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DONRYU; TISSUE=TESTIS;
RX   MEDLINE=98340864; PubMed=9675100;
RA   Maeda T., Sakashita M., Ohba Y., Nakanishi Y.;
RT   "Molecular cloning of the rat Tpx-1 responsible for the interaction
RT   between spermatogenic and sertoli cells.";
RL   Biochem. Biophys. Res. Commun. 248:140-146(1998).
DR   EMBL; AB009662; BAA32029.1; -.
DR   HSSP; P04284; 1CFE.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AGS_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AGS_PR1_SC7_2; 1.
SQ   SEQUENCE 243 AA; 27344 MW; 27A89240EA077CB1 CRC64;

Query Match            59.3%;
Best Local Similarity  61.6%;
Matches  151;   Conservative  31;   Mismatches  61;   Indels  2;   Gaps  2;

                       Score 852;   DB 11;   Length 243;   Pred No. 1.1e-74;

Qy   14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
         | ||| |: ||| ||| ||||:||:|| |: || :| ||||||:|||||||:||||| ::
Db    1 MAWFQVMLFVFAVLLP-LPPTEGKDPDFAFLTFTNQIQVQREIIAKHNELRRQVSPPGSNI 59

Qy   74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
         |||||| :||||||||||:| |  :| :|:|| :||||||||:: :||||:|||||:::|
Db   60 LKMEWNVQAAANAQKWANNCILEHSSTEDRKINIKCGENLYMSTDPTSWRTVIQSWYEEN 119

Qy  134 NDFDFGVGPKTPNAVVGHYTQVVWYSSILVGGGNAYCPNQKVLKYYVCQYCPAGNWANR 193
         ::| |||| : |:||||||||:|||||: ||||:||||||: |||:|||:||| ||| :
Db  120 ENFVFGVGAK-PNSAVGHYTQLVWYSSFKVGCGVAYCPNQDTLKYFYVCHYCPMGNNVMK 178

Qy  194 LYVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNC 253
         | :|| || |||||| ||| || ||||:| | || | ||| | ||| |  ||| :| |
Db  179 KSTPYHQGTPCASCPNNCDNGLCTNSCDFEDLLSNCESLKSSAGCKHELLKAKCEATCLC 238

Qy  254 SNSIY 258
         ::|:
Db  239 EDKIH 243
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RESULT 3
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ID   Q9RIL4        PRELIMINARY;    PRT;   243 AA.
AC   Q9RIL4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich secretory protein-2 crisp-2.
DE   TPX-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=98284327; PubMed=9621307;
RA   O'Bryan M.K., Loveland K.L., Herszfeld D., McFarlane J.R., Hearn M.T.,
RA   de Kretser D.M.;
RT   "Identification of a rat testis-specific gene encoding a potential rat
RT   outer dense fibre protein.";
RL   Mol. Reprod. Dev. 50:313-322(1998).
DR   EMBL; AF078552; AAD48090.1; -.
DR   HSSP; P04284; 1CFE.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AGS_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AGS_PR1_SC7_2; 1.
SQ   SEQUENCE 243 AA; 27429 MW; FA604ECE50F7D3BA CRC64;

Query Match            59.1%;
Best Local Similarity  61.2%;
Matches  150;   Conservative  31;   Mismatches  62;   Indels  2;   Gaps  2;

                       Score 849;   DB 11;   Length 243;   Pred No. 2.2e-74;

Qy   14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
         | ||| |: ||| ||| ||||:||:|| |: || :| ||||||:|||||||:||||| ::
Db    1 MAWFQVMLFVFGVLLP-LPPTEGKDPDFAFLTFTNQIQVQREIIAKHNELRRQVSPPGSNI 59

Qy   74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
         |||||| :||||||||||:| |  :| :|:|| :||||||||:: :||||:|||||:::|
Db   60 LKMEWNVQAAANAQKWANNCILEHSSTEDRKINIKCGENLYMSTDPTSWRTVIQSWYEEN 119

Qy  134 NDFDFGVGPKTPNAVVGHYTQVVWYSSILVGGGNAYCPNQKVLKYYVCQYCPAGNWANR 193
         ::| |||| : |:||||||||:|||||: ||||:||||||: |||:|||:||| ||| :
Db  120 ENFVFGVGAK-PNSAVGHYTQLVWYSSFKVGCGVAYCPNQDTLKYFYVCHYCPMGNNVMK 178

Qy  194 LYVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNC 253
         | :|| || |||||| ||| || ||||:| | || | ||| | ||| |  ||| :| |
Db  179 KSTPYHQGTPCASCPNNCDNGLCTNSCDFEDLLSNCESLKSSARCKHELLKAKCEATCLC 238

Qy  254 SNSIY 258
         ::|:
Db  239 EDKIH 243
```

RESULT 4
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ID   Q91XA3        PRELIMINARY;    PRT;   244 AA.
AC   Q91XA3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Similar to acidic epididymal glycoprotein 1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC011150; AAH11150.1; -.
DR   MGD; MGI:102553; Aeg1.
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DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   PROSITE; PS01009; SCP_AGS_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AGS_PR1_SC7_2; 1.
SQ   SEQUENCE   244 AA;  27622 MW;  BDE122E22E5E8146 CRC64;

Query Match             52.5%;  Score 754.5;  DB 11;  Length 244;
Best Local Similarity   54.3%;  Pred. No. 3.3e-65;
Matches  133; Conservative  39; Mismatches  72; Indels  1; Gaps  1;

Qy     14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHHNELRRAVSPPARNM 73
           | ||| |||| |||| |||| |||| || ||||||||||||| ||||||:||||||| ::
Db      1 MALMLVLFFLAAVLPPSLLQQSSQENRLEKLSTTKMSVPEIVSKHNQLRRWVSPSGSDL 60

Qy     74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
          |||||||| |||:|||  ||||||  :||||||||||:||||||||:|| |||||||||
Db     61 LKMEWNYDAQVNAQQWADKCTFSHSPIELRTTNLRCGENSFMSSYLASWSSAIQGWYNEY 120

Qy    134 NDFDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYIYVCQYCPAGNWANR 193
          ||||| ||| |||||||| |||| |||| | :|||||||||| |||| | ||||||| |
Db    121 KDLTVDVGPKQPDSVVGHYTQVVWNSTFQVACGVAECP-KNPLRYYVCYHCVCPVGNYQGR 179

Qy    194 LYVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNC 253
          | ||:||||||| |||:||||| | |:||| || | |||:|| ||:|:||| |||:| |
Db    180 LYTPYTAGEPCASCPDHCEDGLCTNSCGHEDKXTNCKYLKKMLSCEHELLKKGCKATCLC 239

Qy    254 SNSIY 258
          |:
Db    240 EGKIH 244
```

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RESULT 5
077720
ID   077720;                       PRELIMINARY;      PRT;    165 AA.
AC   077720;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich secretory protein-2 (Fragment).
GN   CRISP-2.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Schambony A., Toepfer-Petersen E.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ006632; CAA07160.1; -.
HSSP; P04284; 1CFE.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01010; SCP_AGS_PR1_SC7_2; 1.
FT   NON_TER       1       1
FT   NON_TER     165     165
SQ   SEQUENCE   165 AA;  18402 MW;  91172E8A7D4680B9 CRC64;

Query Match             47.6%;  Score 684;  DB 6;  Length 165;
Best Local Similarity   69.7%;  Pred. No. 1.4e-58;
Matches  115; Conservative  18; Mismatches  32; Indels  0; Gaps  0;

Qy     69 PARNMLKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQS 128
          || |||||||||||||||||||:|||  |||||||  :||||||||||:||||||||:||
Db      1 PASNMLKMEWSREATANAKRWANKCTLEHSSADDRKTSTRCGENIYMSSDPTPWSDAIQS 60

Qy    129 WFDEYNDFDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYIYVCQYCPAG 188
          |:|| |:||||||| |||||||| |||||| |||||||||| |||||:|||| | |||||||
Db     61 WIDESLDFTYGVGPKSAGSVVGHYTQAVWVSSYRVGCGIAYCPNQESLKYIYVCQYCPVG 120
```

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Qy    189 NWANRLYVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLX 233
          || |||||||||| |||||||| ||  | :|||| |||||| |||
Db    121 NNVNKKNTPYEQGHPCASCPGNCDNGICTNSCEYEDLLSNCDSLK 165
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RESULT 6
Q9N0J2
ID   Q9N0J2;                       PRELIMINARY;      PRT;    151 AA.
AC   Q9N0J2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich secretory protein-2 (Fragment).
GN   CRISP-2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Gentzel M., Schambony A., Toepfer-Petersen E.;
RT   "Identification of CRISP proteins of stallion and bull.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ277708; CAB90614.1; -.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
FT   NON_TER       1       1
FT   NON_TER     151     151
SQ   SEQUENCE   151 AA;  16703 MW;  DA2F1AE692C929E1 CRC64;

Query Match             41.1%;  Score 590.5;  DB 6;  Length 151;
Best Local Similarity   71.7%;  Pred. No. 1.5e-49;
Matches  109; Conservative  16; Mismatches  26; Indels  1; Gaps  1;

Qy     14 MTLFPVLLFLVAGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHHNELRRAVSPPARNM 73
          | || | | ||| |||| |||| |||| || ||||||||||:||||||||||||||||
Db      1 MALLPVVLFLAAVLPSLP-TEGKDPAFSALLTTQTQVQREIVNKINELRKSVSPPASNM 59

Qy     74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
          |||||| |||||||||||||||  :||||||||||:|||||||||||||||||||||||
Db     60 LKMEWSREATANAQKWANKCTLEHSSADDRKTSTRCGENIYMSSDPTPWSDAIQSWIDES 119
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Qy    134 NDFDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGC 165
          |:|||||| |||||||| |||||| ||||||
Db    120 LDFTYGVGPKSAGSVVGHYTQAVWVSSFRVGC 151
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RESULT 7
Q9D259
ID   Q9D259;                       PRELIMINARY;      PRT;    250 AA.
AC   Q9D259;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   SEQUENCE FROM N.A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=C57BL/6J; TISSUE=EPIDIDYMIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
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RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK020340; BAB32077.1; -.
DR MGD; MGI:1925331; 9230112K08Rik.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD005542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
SQ SEQUENCE   250 AA; 28704 MW; 747B45FF2FBDB9D1 CRC64;

Query Match   40.0%; Score 574.5; DB 11; Length 250;
Best Local Similarity   46.1%; Pred. No. 1e-47;
Matches 113; Conservative 35; Mismatches 90; Indels   7; Gaps   5;

Qy   19 VLFLVAGLLPSF---PANEDKDPAFTALLT-TQTQVQREIVNKHNELRRAVSPPARNML 74
             |:| || | :||||| ||| | | |||||:||||||||||||||||||
Db   6 ILLLFVAAFVPVVTIRPLKLDR-ALYNKLITESQTEPQEEIVTHHAFRKVSPPARNML 64

Qy   75 KMEWNKEAAANAQKWANQCNYRHSNPKD--RWTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
          |:||:| || |||||||||||||| |||||||||||||||||||||||||||||
Db   65 KVSWSSAAAENARILARYCDKSDSDSLERRLPNTFCGENMLMEHYPSSMSKVIEIWFNES 124

Qy   134 NDFDFGVGPKTPNAV--VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWAN 192
          |:|| || || | ||||||||||||||:| || ||:||| :||:|| || |||||
Db   125 FRYGLWPSTDDDISTDRYTQIVWARTSYLIGCAIAPCRHRGSPRYFYVCHYCHEGNDPETK 184

Qy   193 RLYVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCN 252
          :|||||||||||| | || ||| | || ||:| || |:| || || ||||||||
Db   185 TLNMPYKEGSPCDDCPNNCEDGLCGTNPCIIYDEYNNCDTQVKLYGCSHPAVQPPCKASCL 244

Qy   253 CSNSI 257
          |::|
Db   245 CTTEI 249

RESULT 8
ID Q9XSD3
AC Q9XSD3;   PRELIMINARY;   PRT;   249 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Androgen-dependent acidic epididymal glycoprotein.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Sivashanmugam P., Richardson R.T., Hall S., Hamil K.G., French F.S.,
RA O'Rand M.G.;
RT "Cloning and characterization of an androgen dependent acidic
RT epididymal glycoprotein/crisp1-like protein from the monkey.";
RL J. Androl. 20:0-0(1999).
DR EMBL; AF123894; AAD27611.1; -.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD005542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
SQ SEQUENCE   249 AA; 26653 MW; 26DD3071C5F1F2A1 CRC64;

Query Match   37.8%; Score 542.5; DB 6; Length 249;
Best Local Similarity   44.9%; Pred. No. 1.3e-44;
Matches 109; Conservative 34; Mismatches 95; Indels   5; Gaps   4;

Qy   20 LLFLVAG--LLPSFP-ANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNML 76
             ||| :| |:|| || ||||||||||||||||||||||||||||
Db   6 LLFLVAAACLLPVLSMRKRSAKKLFNKLVTDLPNVQQEIVNIHNFTLRGVYPPASNMLKM 65

Qy   77 EWNKEAAANAQKWANQCNYRHSNPKD-RWTSLKCGENLYMSSAPSSWSQAIQSWFDEYND 135
          |||:| || | |||||||||||| :||||||||||||||||||||||||:| |
Db   66 SWSEEAAQNAKIFSRYCDMTESNPLERRLPNTFCGENRNMTSYPVSWSSSVIGVWYSESKY 125

Qy   136 FDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWANRL 194
          || ||||| | ||||||||||||||:| || ||||| :||:|| :||||||||:|
Db   126 FRYGLWPSTDDDISTDRYTQIVWARTSYLIGCAIAPCRHRGSPRYFYVCHYCHEGNDPETK 185

Qy   195 YVPYEQGAPCASCPDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNCNS 254
          ||||||||||| | || ||| | || ||:| || |:| || || |||||||| |
Db   186 HEPYKRGVPCEACPNNCEDKLCTNPCIYDEYYDCSLEVRFLGCNHSTPRMPCKACLCD 245

Qy   255 NSI 257
          |
Db   246 TEI 248

RESULT 9
ID O77719
AC O77719;   PRELIMINARY;   PRT;   217 AA.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cysteine-rich secretory protein-1 (Fragment).
GN CRISP-1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EPIDIDYMIS;
RA Schambony A., Toepfer-Petersen E.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ006631; CAA07159.1; -.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD005542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
FT NON_TER   1   1
SQ SEQUENCE   217 AA; 24832 MW; 86AA6778A244CAE8 CRC64;

Query Match   36.6%; Score 525; DB 6; Length 217;
Best Local Similarity   45.4%; Pred. No. 5.5e-43;
Matches 98; Conservative 33; Mismatches 83; Indels   2; Gaps   2;

Qy   44 LLTTQTQVQREIVNKHNELRRAVSPPARNMLKMEWNKEAAANAQKWANQCNYRHSNPKD-- 102
          |: |||||:||:| |||:|||:||||| |||| || |:| || | |||||||||||
Db   1 VLTDLATVQEEIVTVHVNHTLRRRVIPPASNMLKMNWSEEAQNAARLSAQCELSESKALER 60

Qy   103 RMTSLKCGENLYMSSAPSSWSQAIQSWFDEYNDFDFGVGPKTPN-AVVGHYTQVVWYSSY 161
          |:||:|||||||||||||||||||||||:| ||:|| ||||| | ||||||||||||
Db   61 RITNTFCGANMHLTSYPISWSNVIGMWFSESKYFKYGQWISTDDEVIIEHYTQLVWATSY 120

```
Qy   162 LVGGGNAYCPNQKVLKYYYCQYCPAGNWANRLYVPYEQGAPCASCPDNCDDGIGTNGCK 221
         |:||| |||| ||:|||: |||||||:||:: |||||||:|:|||||:||:||
Db   121 LIGCGISSCSKRSTQYLIVYCHYCHEGNDPDKNVPYNMGTPCKCQPNDCEDRLCTNPCL 180

Qy   222 YEDLYSNCKSLKLTLTCKHQLVRDSCKASCNCSNSI 257
         |:|| ||||||:||| |:| ||:|:|
Db   181 YYDESNKCKTQKEALGCSHLSVKLFPCKATCLCDTEI 216
```

RESULT 10
Q8UW11
ID   Q8UW11;   PRELIMINARY;   PRT;   181 AA.
AC   Q8UW11;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich venom protein.
OS   Lapemis hardwickii (Hardwick's sea snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Hydrophiinae; Lapemis.
OX   NCBI_TaxID=8781;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wei J., Zhong X., Yang W., Zhao G., Xu A.;
RT   "A novel cysteine-rich venom protein cDNA from sea snake.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF190861; AAL54918.1; -.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; VSTPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.
DR   PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
SQ   SEQUENCE   181 AA;   20123 MW;   43259925EB307C2 CRC64;

Query Match   36.2%;   Score 520;   DB 13;   Length 181;
Best Local Similarity   46.4%;   Pred. No. 1.3e-42;
Matches   85;   Conservative   35;   Mismatches   59;   Indels   4;   Gaps   2;

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Qy    76 MEWNKEAAANAQKWANQCNYRHSNPKDR-MTSLKCGENLYMSSAPSSWSQAIOSWFDEYN 134
         :|:|| ||  |:|||||||||::||| |  :||:|||||||  ||| ||||||:||:||
Db     1 MKWNSHAAQNAKRSADRCTFAHSPEHTRTVGKFRCGENIFMSSQPFAWSGVVQOAWYDEIK 60

Qy   135 DFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWANRL 194
         :|:||| | |::|||||||::|||:||||||||:||||||:|::||:|||||||||:: :
Db    61 NFVGIGARPPGSVIGHYTQIVWKSHLLGCASAKCSS---TKYLYVCQYCPAGNIRSSI 117

Qy   195 YVPYEQGAPCASCPDNCDDGIGTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKASCNCS 254
         |:|| |::| | |:|:||  | :|:|| |:|||||| ||:|||| ||| |:| ||:|
Db   118 ATPYKSGPSCGDCPSACVNGLCTNPCEYEDAYTNCNDLVKERKCQTEWIKSQCPATCFH 177

Qy   255 NSI 257
         |:|
Db   178 NKI 180
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RESULT 11
Q8UW25
ID   Q8UW25;   PRELIMINARY;   PRT;   199 AA.
AC   Q8UW25;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich venom protein.
OS   Lapemis hardwickii (Hardwick's sea snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Hydrophiinae; Lapemis.
OX   NCBI_TaxID=8781;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wei J., Zhong X., Yang W., Zhao G., Xu A.;
RT   "A Novel Cysteine-Rich Venom Protein Precursor (CRVP) mRNA from Sea
RT   Snake (Lapemis Hardwickii).";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159541; AAL54896.1; -.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; VSTPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; UNKNOWN_1.
DR   PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
SQ   SEQUENCE   199 AA;   21797 MW;   9BBC48B0C51CACE9 CRC64;

Query Match   35.7%;   Score 512.5;   DB 13;   Length 199;
Best Local Similarity   46.6%;   Pred. No. 8e-42;
Matches   96;   Conservative   35;   Mismatches   66;   Indels   9;   Gaps   3;

```
Qy    14 MTLFPVLFLVAGILPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPARNM 73
         :| |:||:|:|:|    |:|      |:   :| ||::|||::|||:|||:||:|::|||
Db     1 MIAFIVLLSLAAVLQQVSGGTVD-----FASESSNKKDYRREIVDKHNALRRSVKPTARNM 55

Qy    74 LKMEWNKEAAANAQKWANQCNYRHSNPKDR-MTSLKCGENLYMSSAPSSWSQAIQSWFDE 132
         |: :|:|| ||  |:|||||||::||| |  :||:|||||||  ||| ||||||:||:
Db    56 LQMKWNSRAAQNAKRSADRCTFAHSPEHTRTVGKFRCGENIFMSSQPFAWSGVVQOWYDE 115

Qy   133 YNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYCPAGNWAN 192
         :  :|:||| | |::|||||||::|||:||||||||:||||||:|::||:|||||||||:
Db   116 IKNVVDGIGARPPGSVIGHYTQIVWKSHLLGCASAKCSS---TKYLYVCQYCPAGNISS 172

Qy   193 RLYVPYEQGAPCASCPDNCDDGIGTN 218
         :|:|| ||:|:||  | :|||||
Db   173 SIATPYKSGPSCGDCPSACVNGLCTN 198
```

RESULT 12
Q9N0J1
ID   Q9N0J1;   PRELIMINARY;   PRT;   111 AA.
AC   Q9N0J1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cysteine-rich secretory protein-1 (Fragment).
GN   CRISP-1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=EPIDYDIMIS;
RA   Gentzel M., Schambony A., Toepfer-Petersen E.;
RT   "Identification of CRISP proteins of stallion and bull.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ277709; CAB90615.1; -.
DR   HSSP; P04204; 1CFE.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; VSTPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
SQ   SEQUENCE   111 AA;   12284 MW;   B5438EA103C0B941 CRC64;

Query Match   32.2%;   Score 463;   DB 6;   Length 111;
Best Local Similarity   69.4%;   Pred. No. 2.5e-37;
Matches   77;   Conservative   12;   Mismatches   22;   Indels   0;   Gaps   0;

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Qy   148 VVGHYTQVVWYSSYLVGGGNAYCPNQKVLKYYYVCQYCPAGNWANRLYVPYEQGAPCASC 207
         |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
```

Db   1 VVGHYTQVVWYSSYRVCGGIAYCPNQENLKYYVCQYCPAGNNYSKKNTPYKEGTPCASC 60

Qy   208 PDNCDDGLCTNGCKYEDLYSNCKSLKLTLTCKHQLVRDSCKSASCNCSNSIY 258
           |:||||||| || || || ||
Db   61 PGDCDDGLCTNTCQYEDLLSNCDSLKKTAGCGHELLKEKCKATCLCEGRIY 111

RESULT 13
Q9R0V8
ID   Q9R0V8   PRELIMINARY;   PRT;   158 AA.
AC   Q9R0V8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Acidic epididymal glycoprotein D/E (Fragment).
GN   CRISP-1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RA   Klemme L.M., Siiteri J.E., Hamilton D.W.;
RT   "The Rat Androgen-Regulated Acidic Epididymal Protein D (rCrisp-1).
RT   Gene: Structural Comparison with Other Crisp Genes, Identification of
RT   Alternative Transcripts and of Transcriptional Regulatory Elements.";
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U60956; AAD41529.1; -.
DR   EMBL; U60953; AAD41529.1; JOINED.
DR   EMBL; U60954; AAD41529.1; JOINED.
DR   EMBL; U60955; AAD41529.1; JOINED.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
NON_TER   1
NON_TER   158
SQ   SEQUENCE   158 AA;   17975 MW;   26E53DAB08798EA1 CRC64;

Qy   16 LFPVLLFLVAGLLPSF--PANEDKDPAFTALLITQTQVQREIVNKHNELRRAVSPPARNM 73
           : ||| |||| | || ||||||||||||||||||||||:|||||||||| | ||
Db   2 LMLVLLFLAAVLPPSLLQDTTDEWDRDLENLSTTKLSVQEEIINKHNQLRRTVSPSGSDL 61

Qy   74 LKMEWNKEAAANAQKWANQCNYRHSNPKDRMTSLKCGENLYMSSAPSSWSQAIQSWFDEY 133
           | |:|| |||||| |||||||||||||||||||||||||||||||||:||||||:|||
Db   62 LRVEWDHDAYVNAQKWANRCIYINHSPLQHRTTLKCGENLFMANYPASWSSVIQDWYDES 121

Qy   134 NDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYC 170
           |:| ||||||||||| |||||||||||:|| ||||||
Db   122 LDFVPFGPKVGVKVGHYTQVVWNSTFLVACGVAEC 158

Query Match   30.6%;   Score 440;   DB 11;   Length 158;
Best Local Similarity   54.1%;   Pred. No. 6.6e-35;
Matches 85;   Conservative 21;   Mismatches 49;   Indels 2;   Gaps 1;

RESULT 14
Q96SF6
ID   Q96SF6   PRELIMINARY;   PRT;   178 AA.
AC   Q96SF6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   AEGL1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]

RP   SEQUENCE FROM N.A.
RA   Williams S.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL359458; CAC34981.1; -.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
SQ   SEQUENCE   178 AA;   20462 MW;   18739B2B6EBF7F84 CRC64;

Qy   81 LLFLVAG--LLP--SFPANEDKDPAFTALLITQTQVQREIVNKHNELRRAVSPPARNMLK 75
           ||||||| ||| |:| ||||||||||||||||||||||| ||| | ||| ||
Db   6 LLFLVAAACLLPMLSMKKKSARD-QFNKLVTDLPNVQEEIVNIHHALRRYVPPASNMLK 64

Qy   76 MEWNKEAAANAQKWANQCNYRHSNPKD-RMTSLKCGENLYMSSAPSSWSQAIQSWFDEYN 134
           |:|| | :||| ||||:|||||||||| ||||||||:||||||||||||||:||||| |
Db   65 MSWSEEAAQNARIPSKYCDMTESNPLERRLPNTFCGENMHMTSYPVSWSSVIGVWYSEST 124

Qy   135 DFDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYVCQYC 185
           |:| ||||||| || ||||||||:||||||||||||||||||:||:|| |
Db   125 SFKHGEWTTTDDIITTDHYTQIVWARSYLIGCAIASCRQQSSPRLYCVCHYC 176

RESULT 15
Q90XE5
ID   Q90XE5   PRELIMINARY;   PRT;   153 AA.
AC   Q90XE5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Allurin (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21457293; PubMed=11562501;
RA   Olson J.H., Xiang X., Ziegert T., Kittelson A., Rawls A., Bieber A.L.,
RA   Chandler D.E.;
RT   "Allurin, a 21-kDa sperm chemoattractant from Xenopus egg jelly, is
RT   related to mammalian sperm-binding proteins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:11205-11210(2001).
DR   EMBL; AF393653; AAL12003.1; -.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1.
DR   PROSITE; PS01010; SCP_AG5_PR1_SC7_2; UNKNOWN_1.
NON_TER   1
SQ   SEQUENCE   153 AA;   17684 MW;   E01A2467885FC36CA CRC64;

Qy   135 DFDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYVCQYC 185
           | |:|| || |:| |||||||||||||||:||||||||||||||||| |
Db   125 SFKHGEWTTTDDIITTDHYTQIVWARSYLIGCAIASCRQQSSPRLYCVCHYC 176

Query Match   26.0%;   Score 373.5;   DB 4;   Length 178;
Best Local Similarity   47.1%;   Pred. No. 2.2e-28;
Matches 81;   Conservative 21;   Mismatches 63;   Indels 7;   Gaps 5;

Qy   20 LLFLVAG--LLP--SFPANEDKDPAFTALLITQTQVQREIVNKHNELRRAVSPPARNMLK 75
           ||||||| ||| |:| ||||||||||||||||||||||| ||| | ||| ||
Db   6 LLFLVAAACLLPMLSMKKKSARD-QFNKLVTDLPNVQEEIVNIHHALRRYVPPASNMLK 64

Qy   76 MEWNKEAAANAQKWANQCNYRHSNPKD-RMTSLKCGENLYMSSAPSSWSQAIQSWFDEYN 134
           |:|| | :||| ||||:|||||||||| ||||||||:||||||||||||||:||||| |
Db   65 MSWSEEAAQNARIPSKYCDMTESNPLERRLPNTFCGENMHMTSYPVSWSSVIGVWYSEST 124

Qy   135 DFDFGVGPKTPNAV-VGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYVCQYC 185
           |:| ||||||| || ||||||||:||||||||||||||||||:||:|| |
Db   125 SFKHGEWTTTDDIITTDHYTQIVWARSYLIGCAIASCRQQSSPRLYCVCHYC 176

Qy   72 NMLKMEWNKEAAANAQKWANQCNYRHSNPKDR----MTSLKCGENLYMSSAPSSWSQAIQ 127
           :| ||:|| | |||||||| |:|||||||||| |||||||::|||||||||||||:
Db   1 DMKKMVWCDPAALNAYNFATQCSMHSLVEERHIKEPIDVVCGENIYMSTAKSDWSTVID 60

Qy   128 SWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYVCQYCPA 187
           :||:|::| :|| || |:| |||||||||||||||:||||||||||||||||||||||
Db   61 SWYNERSDFAYGKG-KISDKPIGHYTQVVWAKSYLLGCAYNFCKENK-YPHVEVCHYGPM 118

Query Match   24.9%;   Score 358;   DB 13;   Length 153;
Best Local Similarity   46.3%;   Pred. No. 5.8e-27;
Matches 69;   Conservative 22;   Mismatches 52;   Indels 6;   Gaps 3;

Qy   188 GNWANRLYVPYEQGAPCASCPDNCDDGLC 216
           | ||||| :||:|| ||||||:||| |||
Db   119 GNMDESVPRPYEBGEWCASCPESCDDKLC 147

Search completed: March 14, 2003, 05:42:59
Job time : 52.2472 secs